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RAW SEQUENCE LISTING

DATE: 11/26/2001

PATENT APPLICATION: US/09/919,835

TIME: 12:14:30

Input Set : A:\211710US0X.txt.

Output Set: N:\CRF3\11212001\I919835.raw

ENTERED

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3 <110> APPLICANT: BATHE, BRIGITTE
4      MOECKEL, BETTINA
5      PFEFFERLE, WALTER
6      HUTHMACHER, KLAUS
7      RUECKERT, CHRISTIAN
8      KALINOWSKI, JOERN
9      PUEHLER, ALFRED
10     BINDER, MICHAEL
11     GREISSINGER, DIETER
12     THIERBACH, GEORG
14 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METE GENE
16 <130> FILE REFERENCE: 211710US0X
18 <140> CURRENT APPLICATION NUMBER: 09/919,835
19 <141> CURRENT FILING DATE: 2001-08-02
21 <150> PRIOR APPLICATION NUMBER: DE 10038023.9
22 <151> PRIOR FILING DATE: 2000-08-02
24 <150> PRIOR APPLICATION NUMBER: DE 10109689.5
25 <151> PRIOR FILING DATE: 2001-02-28
27 <150> PRIOR APPLICATION NUMBER: US 60/294,250
28 <151> PRIOR FILING DATE: 2001-05-31
30 <160> NUMBER OF SEQ ID NOS: 8
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2810
36 <212> TYPE: DNA
37 <213> ORGANISM: Corynebacterium glutamicum
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (317)..(2551)
42 <223> OTHER INFORMATION:
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46 agcccaaac ggcacatga atttaaattc ccggaacttc ttgacagacc gagcagtcta      60
48 gggtttggtt gaaaacgcaa tcggttcact ttaaatcctc tcctggagc cccggatgat      120
50 gaggaacgcc aaagctttct gaatggaaat ttaagcggtt aagtgggacg acctcgatta      180
52 caaaaaggcg aggaaacccc cggggcagct ttctgccacc cgtgatttc gcgaaccttg      240
54 aaacatcgtc agaagattgc cgtgcgtcct agccgggata cgcacgttcg gctcaagcag      300
56 aaagtcttta actcac atg act tcc aac ttt tct tcc act gtc gct ggt ctt      352
57           Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu
58           1             5             10
60 cct cgc atc gga gcg aag cgt gaa ctg aag ttc gcg ctc gaa ggc tac      400
61 Pro Arg Ile Gly Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr
62           15             20             25
64 tgg aat gga tca att gaa ggt cgc gaa ctt gcg cag acc gcc cgc caa      448
65 Trp Asn Gly Ser Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln
66           30             35             40
68 ttg gtc aac act gca tcg gat tct ttg tct gga ttg gat tcc gtt ccg      496
69 Leu Val Asn Thr Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro

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70	45	50	55	60	
72	ttt gca gga cgt tcc tac tac gac gca atg ctc gat acc gcc gct att				544
73	Phe Ala Gly Arg Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile				
74		65	70	75	
76	ttg ggt gtc ctg ccg gag cgt ttt gat gac atc gct gat cat gaa aac				592
77	Leu Gly Val Leu Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn				
78		80	85	90	
80	gat ggt ctc cca ctg tgg att gac cgc tac ttt ggc gct gct cgc ggt				640
81	Asp Gly Leu Pro Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly				
82		95	100	105	
84	act gag acc ctg cct gca cag gca atg acc aag tgg ttt gat acc aac				688
85	Thr Glu Thr Leu Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn				
86		110	115	120	
88	tac cac tac ctc gtg ccg gag ttg tct gcg gat aca cgt ttc gtt ttg				736
89	Tyr His Tyr Leu Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu				
90	125	130	135	140	
92	gat gcg tcc gcg ctg att gag gat ctc cgt tgc cag cag gtt cgt ggc				784
93	Asp Ala Ser Ala Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly				
94		145	150	155	
96	gtt aat gcc cgc cct gtt ctg gtt ggt cca ctg act ttc ctt tcc ctt				832
97	Val Asn Ala Arg Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu				
98		160	165	170	
100	gct cgc acc act gat ggt tcc aat cct ttg gat cac ctg cct gca ctg				880
101	Ala Arg Thr Thr Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu				
102		175	180	185	
104	ttt gag gtc tac gag cgc ctc atc aag tct ttc gat act gag tgg gtt				928
105	Phe Glu Val Tyr Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val				
106		190	195	200	
108	cag atc gat gag cct gcg ttg gtc acc gat gtt gct cct gag gtt ttg				976
109	Gln Ile Asp Glu Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu				
110	205	210	215	220	
112	gag cag gtc cgc gct ggt tac acc act ttg gct aag cgc gat ggc gtg				1024
113	Glu Gln Val Arg Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val				
114		225	230	235	
116	ttt gtc aat act tac ttc ggc tct ggc gat cag gcg ctg aac act ctt				1072
117	Phe Val Asn Thr Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu				
118		240	245	250	
120	gcg ggc atc ggc ctt ggc gcg att ggc gtt gac ttg gtc acc cat ggc				1120
121	Ala Gly Ile Gly Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly				
122		255	260	265	
124	gtc act gag ctt gct gcg tgg aag ggt gag gag ctg ctg gtt gcg ggc				1168
125	Val Thr Glu Leu Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly				
126		270	275	280	
128	atc gtt gat ggt cgt aac att tgg cgc acc gac ctg tgt gct gct ctt				1216
129	Ile Val Asp Gly Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu				
130	285	290	295	300	
132	gct tcc ctg aag cgc ctg gca gct cgc ggc cca atc gca gtg tct acc				1264
133	Ala Ser Leu Lys Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr				
134		305	310	315	

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136 tct tgt tca ctg ctg cac gtt cct tac acc ctc gag gct gag aac att      1312
137 Ser Cys Ser Leu Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile
138              320              325              330
140 gag cct gag gtc cgc gac tgg ctt gcc ttc ggc tcg gag aag atc acc      1360
141 Glu Pro Glu Val Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr
142              335              340              345
144 gag gtc aag ctg ctt gcc gac gcc cta gcc ggc aac atc gac gcg gct      1408
145 Glu Val Lys Leu Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala
146              350              355              360
148 gcg ttc gat gcg gcg tcc gca gca att gct tct cga cgc acc tcc cca      1456
149 Ala Phe Asp Ala Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro
150 365              370              375              380
152 cgc acc gca cca atc acg cag gaa ctc cct ggc cgt agc cgt gga tcc      1504
153 Arg Thr Ala Pro Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser
154              385              390              395
156 ttc gac act cgt gtt acg ctg cag gag aag tca ctg gag ctt cca gct      1552
157 Phe Asp Thr Arg Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala
158              400              405              410
160 ctg cca acc acc acc att ggt tct ttc cca cag acc cca tcc att cgt      1600
161 Leu Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg
162              415              420              425
164 tct gct cgc gct cgt ctg cgc aag gaa tcc atc act ttg gag cag tac      1648
165 Ser Ala Arg Ala Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr
166              430              435              440
168 gaa gag gca atg cgc gaa gaa atc gat ctg gtc atc gcc aag cag gaa      1696
169 Glu Glu Ala Met Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu
170 445              450              455              460
172 gaa ctt ggt ctt gat gtg ttg gtt cac ggt gag cca gag cgc aac gac      1744
173 Glu Leu Gly Leu Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp
174              465              470              475
176 atg gtt cag tac ttc tct gaa ctt ctc gac ggt ttc ctc tca acc gcc      1792
177 Met Val Gln Tyr Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala
178              480              485              490
180 aac ggc tgg gtc caa agc tac ggc tcc cgc tgt gtt cgt cct cca gtg      1840
181 Asn Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val
182              495              500              505
184 ttg ttc gga aac gtt tcc cgc cca gcg cca atg act gtc aag tgg ttc      1888
185 Leu Phe Gly Asn Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe
186              510              515              520
188 cag tac gca cag agc ctg acc cag aag cat gtc aag gga atg ctc acc      1936
189 Gln Tyr Ala Gln Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr
190 525              530              535              540
192 ggt cca gtc acc atc ctt gca tgg tcc ttc gtt cgc gat gat cag ccg      1984
193 Gly Pro Val Thr Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro
194              545              550              555
196 ctg gct acc act gct gac cag gtt gca ctg gca ctg cgc gat gaa att      2032
197 Leu Ala Thr Thr Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile
198              560              565              570
200 aac gat ctc atc gag gct ggc gcg aag atc atc cag gtg gat gag cct      2080

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201 Asn Asp Leu Ile Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro
202          575          580          585
204 gcg att cgt gaa ctg ttg ccg cta cga gac gtc gat aag cct gcc tac      2128
205 Ala Ile Arg Glu Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr
206          590          595          600
208 ctg cag tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc      2176
209 Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro
210 605          610          615          620
212 gac gac gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa      2224
213 Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu
214          625          630          635
216 gtg atc tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa      2272
217 Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu
218          640          645          650
220 gca gca cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc      2320
221 Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly
222          655          660          665
224 ttc gag ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc      2368
225 Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg
226          670          675          680
228 gtt cct tcc gcg cag gaa gtg gac ggt ctc ctc gag gct gca ctg cag      2416
229 Val Pro Ser Ala Gln Glu Val Asp Gly Leu Leu Glu Ala Ala Leu Gln
230 685          690          695          700
232 tcc gtg gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag      2464
233 Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
234          705          710          715
236 acc cgt gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag      2512
237 Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu
238          720          725          730
240 tcc gct aag cag gct cgt gag aaa atc gga gca act atc taaattgggt      2561
241 Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
242          735          740          745
244 taccgctagg aaccctaaaga ttaagggcac gagtgtcacc aggattgccg caccatggc      2621
246 aacaccgaag gacaccgtgc ccactcctat ttgcatcaca gcgccaagg tagcggcgcc      2681
248 caaaacagcg cccacctggc gtgaggtgtt gtaaaaacca gaagcagagc ccactaaatc      2741
250 ctgcggaaca tcacgcagag caatcacaga gttcgtgca aaactcatcg cgttgagct      2801
252 accgaacaa      2810
255 <210> SEQ ID NO: 2
256 <211> LENGTH: 745
257 <212> TYPE: PRT
258 <213> ORGANISM: Corynebacterium glutamicum
260 <400> SEQUENCE: 2
262 Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
263 1          5          10          15
266 Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
267          20          25          30
270 Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
271          35          40          45
274 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg

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275      50      55      60
278 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
279 65      70      75      80
282 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
283      85      90      95
286 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
287      100      105      110
290 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
291      115      120      125
294 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
295      130      135      140
298 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
299 145      150      155      160
302 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
303      165      170      175
306 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
307      180      185      190
310 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
311      195      200      205
314 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
315      210      215      220
318 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
319 225      230      235      240
322 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
323      245      250      255
326 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
327      260      265      270
330 Ala Ala Trp Lys Gly Glu Glu Leu Val Ala Gly Ile Val Asp Gly
331      275      280      285
334 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
335      290      295      300
338 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
339 305      310      315      320
342 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
343      325      330      335
346 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
347      340      345      350
350 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
351      355      360      365
354 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
355      370      375      380
358 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
359 385      390      395      400
362 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
363      405      410      415
366 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
367      420      425      430
370 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Ala Met
371      435      440      445

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VERIFICATION SUMMARY

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